# **AMENDMENTS TO THE SPECIFICATION**

Please amend the specification as follows:

Page 1, after the Title and before line 1, insert

# STATEMENT OF GOVERNMENT INTEREST

This invention was made with support pursuant to National Institutes of Health Grant No. RO1 AI29471. The government may have certain rights in this invention.

# **CROSS-REFERENCE TO RELATED APPLICATIONS**

This Application is a Divisional of Application No. 09/453,313, filed December 2, 1999; which is a Continuation-in-Part Application of U.S. Application No. 09/204,117, filed December 2, 1998 (now U.S. Patent 6,413,768), and also claims priority to U.S. Provisional Application No. 60/158,738, filed October 12, 1999; the above noted prior applications are all hereby incorporated by reference.

# At page 15, the paragraph encompassing lines 17-18 is amended as follows:

Figure 3<u>A-H</u>: Flow cytometry histograms of GFP fluorescence for CVD 908-htrA carrying expression vectors with the hok-sok post-segregational killing system.

# At page 15, the paragraph encompassing line 19 is amended as follows:

Figures 4A-<u>DB</u>: <u>Complete pGEN2</u> nucleotide sequence <u>(SEQ ID NO: 1)</u>, <u>comprising nucleotides 1-41964199</u>.

#### At page 15, the paragraph encompassing line 20, is amended as follows:

Figures Figure-5A-B: Partial pGEN3 nucleotide sequence (SEQ ID NO: 2), comprising nucleotides 1201-2397 2400 and showing the sequence of *ori*15A.

### At page 15, the paragraph encompassing line 21 is amended as follows:

<u>Figures Figure-6A-C</u>: <u>Partial pGEN4</u> nucleotide sequence (<u>SEQ ID NO: 3</u>), <u>comprising</u> <u>nucleotides 1201-38483850</u> <u>and showing the sequence of *ori*101.</u>

#### At page 15, the paragraph encompassing lines 24-25 is amended as follows:

<u>Figure-8A-C</u>: Flow cytometry histograms of GFP fluorescence for expression plasmids pGEN91, pGEN111, pGEN121, pGEN193, and pGEN222.

# At page 23, the paragraph encompassing lines 16-18 is amended as follows:

The basic structure of these vectors is represented in Figure 1, and the composite gene sequence for the vector pGEN 2pGEN2 (SEQ ID NO: 1) is represented in Figure 4; Figures 5 & 6 show specific composite sequences for the origins of replication in pGEN3 and pGEN4 respectively.

# At page 43, the paragraph encompassing lines 7-22 is amended as follows:

These data clearly show that when driving expression of gfpuv within the live vector strain CVD 908-htrA,  $P_{ompCI}$  and  $P_{ompC3}$  are inducible with increasing osmolarity, although the basal level of transcription is still noteworthy in both cases. The results observed under conditions of low osmolarity further support our observations using solid media that  $P_{ompCI}$  drives higher heterologous antigen expression than  $P_{ompC3}$ . Since  $P_{ompC3}$  was noted to possess the intended 3'-terminal BgIII site, which was not detected for  $P_{ompCI}$ , we determined the nucleotide sequence for  $P_{ompCI}$  to perhaps detect point mutation(s) which might explain the strength of  $P_{ompCI}$ . The only differences identified were located at the 3'-terminus of the cassette. The intended sequence within this region was 5'-...catataacAGATCTtaatcatccacAGGAGGatatctgATG-3' (SEQ ID NO: 4) (from left to right, upper case denotes the BgIII site, ribosome binding site, and GFPuv start codon respectively); the actual sequence proved to be

5'-...catataacAGATCGATCT taaAcatccacAGGAGGAtAtctgATG-3 (SEQ ID NO: 5) (inserted or changed bases denoted with underlined bold upper case). These changes detected within the ompC1 promoter sequence are apparently responsible for increasing the observed strength of  $P_{ompC1}$  by an unknown mechanism, since neither the basic ompC promoter sequence, nor the optimized ribosome binding site have been spontaneously altered.

# At page 50, lines 6-28 is amended as follows:

#### PRIMER 1:

5'-gaattcGCGCGCTTCGCGATTCAGTCGCGTTCCTTCACA GCTGGCGCAGGGGCGATTACTGATGAA-3' (SEQ ID NO: 6)

#### PRIMER 2:

5'-cccggGAGTCTCCTGAATACGTTTCATAAAAGTGTAA
ACGCGTGAGTGTACCATTTCCACGTAGC-3' (SEQ ID NO: 7)

### PRIMER 3:

5'-cccggGTAAAAACTCAAAGCGTTATTTGCATTTTCGC
TATAGTTCTCGTCTGCTGAAATGCCTGGTGT-3' (SEQ ID NO: 8)

#### PRIMER 4:

5'-gaattcCATTTCTATCAATAAATTACTATTAGTTTTGTCT
TCTAACCAAGCCTCTATTTTATGAGTATCCTCTTCAG-3' (SEQ ID NO: 9)

#### PRIMER 5:

5'-gctagcATGGCCAGCAGAGGCGTAAACAAGGTGATTCT
CGTTGGTAATCTGGGCCAGGACCCGGAAGTACGC-3' (SEQ ID NO: 10)

# PRIMER 6:

# At pages 56, after line 6 to Page 58, line 5 (Table 9), is amended as follows:

TABLE 9							
Primer number	Sequence <sup>1</sup>	Cassette created	GenBank Accession Number	Region of Homology <sup>2</sup>	Region of Complementarity <sup>3</sup>		
1	5'-GCAGGAAAGAACATGTGAG <u>CCTAGG</u> GCCAGCAAAAGGCCA GGAAC-3' (SEQ ID NO:12)	oriE1	J01749	2463-2507			
2	5'-CATGACCAAAATCCCTTA ACTAGTGTTTTAGATCTACT GAGCGTCAGAC CCCG-3' (SEQ ID NO: 13)	66			3197-3145		
3	5'-CGGGGTCTGACGCTCAGT AGATCTAAAACACTAGTTAA GGGATTTTGGTCATG-3' (SEQ ID NO: 14)	bla		3145-3197			
4	5'-GCTGTCAAACATGA <u>GAA</u> <u>TTCTAGA</u> AGACGAAAGGGC  CTCGTGATACGCC-3' ( <u>SEQ ID</u> NO: 15)	66			17 - 1, 4361-4330		
5	5'-ACAGCCTGCAGACAG ATCTTGACAGCTGGATCG CACTCTGGTATAATTGGG AAGCCCTGCAAAG -3' (SEQ ID NO: 16)	aphA-2	V00618	1-64			
6	5'-CGAAGCCCAACCTTTCAT AGAA <u>GCTAGC</u> GGT <u>GGATCC</u> GAAATCTCGTGATGGCAGGT TG-3' (SEQ ID NO: 17)	66	"		1044-986		

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7	5'-AACAAGCGTTATAG <u>GAA</u> TTCTGTGGTAGCA-3' (SEQ ID	PompC	K00541	4 - 33	
	NO: 18)				
'	5'-ACTTTCATGTTATTAAAGA	44			409 460
8					498-469
	TCTGTTATATG-3' (SEQ ID NO:				
	<u>19)</u>				
9	5'-AGATCTTAATCATCCACAG	gfpuv	U62636	289 - 317	
	GAGGCTTTCTGATGAGTAAA				
	GGAGAAGAACTTTTCAC				
	TGG-3' (SEQ ID NO: 20)				
10	5'-GCTAGCTCATTATTTGT				1008-983
10					1000-903
	AGAGCTCATCCATGC-3' (SEQ				
	<u>ID NO: 21)</u>				
11	5'-AGATCTGAATTCTAGAT	tetA	J01749	4 - 41	
	CATGTTTGACAGCTTATCAT				
	CGATAAGCTTTAATGCG-3'				
	(SEQ ID NO: 22)				
12	5'-AGATCTTATCAGGTCGAG	"			1275-1234
12	GTGGCCGGCTCCATGCACC				1273 1254
1					
	GCGACGCAACGCG-3' (SEQ ID				
I <u></u>	NO: 23)	ļ.,	ļ		
13	5'-CGCGAATTCTCGAGACAA	hok-sok-	X05813	2 - 48	
	ACTCCGGGAGGCAGCGTGAT	tetA			
	GCGGCAACAATCACACGGAT				
	TTC-3' (SEQ ID NO: 24)		1		
14	5'-ATGAGCGCATTGTTAGA	"	J01749,		108 - 86,
1 .	TTTCATTTTTTTTCCTCCTT		X05813		580 - 559
	ATTTCTAGACAACATCAGC	Ì	1105015		300 337
	AAGGAGAAAGG -3' (SEQ ID				
I	NO: 25)				
15	5'-CCTTTCTCCTTGCTGAT	"	X05813,	559 - 580,	
	GTTG <u>TCTAGA</u> AAATA <i>AGG</i>		J01749	86 - 108	
	<i>AGG</i> AAAAAAA <i>ATG</i> AAAT				
	CTAACAATGCGCTCAT-3' (SEQ				
	ID NO: 26)				
16	5'-GCTACATTTGAAGAGAT	ori15A	X06403		1461-1397
10	AAATTGCACTGGATCCTAG			1	
	AAATATTTTATCTGATTAA				
1	TAAGATGATC-3' (SEQ ID NO:				
1	27)	46		1700 000	
17	5'-CGGAGATTTCCTGGAA	"	"	780 - 829	
	GATG <u>CCTAGG</u> AGATACTT			1	
.1	AACAGGGAAGTGAGAG-3'				
	(SEQ ID NO: 28)				
18	5'-GTCTGCCGGATTGCTTA	ori101	X01654	4490-4550	
	TCCTGGCGGATCCGGTTGA				
	CAGTAAGACGGGTAAGCCT			1	
1	GTTGAT-3' (SEQ ID NO: 29)			1	
I <u> </u>	1 0110A1-3 (3DQ ID NO. 29)				L

19	5'- <u>CCTAGG</u> TTTCACCTGTT CTATTAGGTGTTACATGCTG TTCATCTGTTACATTGTCGAT CTG-3' (SEQ 1D NO: 30)	•			6464-6408
20	5'-AGGCTTAAGTAGCACCC TCGCA <u>AGATCT</u> GGCAAATC GCTGAATATTCCTTTTGTC TCCGAC-3' (SEQ ID NO: 31)	par	X01654		4918-4858
21	5'-GAGGGCGCCCCAGCTGG CAAT <u>TCTAGACTCGAG</u> CAC TTTTGTTACCCGCCAAACA AAACCCAAAAACAAC-3' (SEQ ID NO: 32)	aphA2- parA	V00618, X04268	38 - 16, 1 - 37	
22	5'-AGAAGAAAAATC <u>GAATTC</u> CAGCATGAAGAGTTTCAGAA AATGACAGAGCGTGAGCAA GTGC-3' (SEQ ID NO: 33)	"	X04268		1704-1644
23	5'-CGAAGCCCAACCTTTCA TAGAA <u>ACTAGT</u> GGTGGAA TCGAAATCTCGTGATGGCA GGTTG-3' (SEQ ID NO: 34)	"	V00618		1044 - 986
24	5'-GTTGTTTTTGGGTTTTGTT TGGCGGGTAACAAAAGTGC TCGAGTCTAGAATTGCCAGC TGGGGCGCCCTC-3' (SEQ ID NO: 35)	66	X04268, V00618	37 - 1, 16 - 38	